

SEQUENCE LISTING

<110> University of North Carolina-Chapel Hill
Elkins, Christopher

<120> Isolated Polynucleotides Encoding DsrA, A Protein Conferring
Serum Resistance To *H. ducreyi*, And Methods And Compositions Comprising
The Same

<130> 5470-269.WO

<160> 18

<170> PatentIn version 3.1

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<212> DNA

<213> *Haemophilus ducreyi*

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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
 85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
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Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val

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Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His Asp Val Pro Pro
85 90 95

Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr
180 185 190

Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly
195 200 205

Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys
 210 215 220

Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr
 225 230 235 240

Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr
 245 250 255

Gly Ala Ser Val Gly Tyr Glu Phe
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His Asp Val Pro Pro
85 90 95

Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr
180 185 190

Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly
195 200 205

Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys
210 215 220

Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr
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Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr
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Gly Ala Ser Val Gly Tyr Glu Phe
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
 85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
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Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
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Asn Thr

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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
 85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
 210 215 220

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
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Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
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Phe

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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
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 35 40 45

Glu Lys Asp Gly Phe Asp Ile Lys Ala Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Lys Trp Ile Ser Arg Gln Ala Thr Tyr Leu Gly Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Ser Ala Glu Pro Asn
85 90 95

Thr Val Leu Leu Tyr Pro Met Pro Asp Pro Asp Gln Leu Gly Ile Asn
100 105 110

Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu Arg
115 120 125

His Gly Phe Lys Leu Asn Val Leu Asp Ala Arg Ile Ser Gln Asn Lys
130 135 140

Gln Asn Ile Asp Thr Ile Ser Glu Tyr Leu Leu Lys Leu Gly Thr Tyr
145 150 155 160

Leu Asp Ser Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile Asn
165 170 175

Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly
180 185 190

Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val
195 200 205

Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr
210 215 220

Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala
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245 250 255

Ala Ser Val Gly Tyr Glu Phe
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<212> DNA
<213> Haemophilus ducreyi

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Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala Pro Asp Val Pro Pro
85 90 95

Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys
180 185 190

Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala Leu Ser
195 200 205

Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser Ala Ala
210 215 220

Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val Gly Ser
225 230 235 240

Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe Asn Thr
245 250 255

Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu Phe
260 265 270

<210> 15
<211> 1047
<212> DNA
<213> Haemophilus ducreyi

<400> 15
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 taaatattta ctagaactgg gtacttattt agatgggtct tatcgtatga tggaacaaaa 660
 tacacataat atcaataaaa atacacataa tatcaataaa aatacacata atatcaataa 720
 gttgtctaaa gaattgcaaa ctggtttagc caaccaatca gcattgtcta tgttagtga 780
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 tgcattagcc attggtgtcg gctcacgcac tactgatcgc tttaccgcta aagcgggtgt 900
 agcgttcaat acctacaatg gcggcatgtc ttatggtgct tctgttggtt atgaattcta 960
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 <211> 273
 <212> PRT
 <213> Haemophilus ducreyi

<400> 16

Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala Pro Asp Val Ser Pro
 85 90 95

Ser Ser Ile Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu
 100 105 110

Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn
 115 120 125

Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser
 130 135 140

Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu
 145 150 155 160

Gly Thr Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln Asn Thr His
 165 170 175

Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile
 180 185 190

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 195 200 205

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 210 215 220

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
 225 230 235 240

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
 245 250 255

Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
 260 265 270

Phe

<210> 17
 <211> 1189
 <212> DNA
 <213> Haemophilus ducreyi

<400> 17
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 ttacttaatg aggtgattat gaaaattaaa tgtttagttg ccgtagtggtg attagcttgt 180

tctactatta caacaatggc tcagcagccg ccaaagtttg ctggagtatc ttctttgtat 240
agctatgagt atgactatgg taagggtaaa tggacttggc ctaatgaagg cggtttcgat 300
attaaagtgc cagggattaa aatgaagcca aaagaatgga tttctaaaca ggctacttat 360
cttgaattac agcattatat gccttatact cctgttctcg tgacatatgc tcttggcggt 420
tctoctagcc ctatactggt atatccgatg tctgatcctg atcaacttgg aataaatcgg 480
cagcagctga aattgaattt gtatagttat tttaacgatt taagacacga ttttaaatta 540
aaagttcttg atgcacgtat ttccaaaaat aaacaaaata ttgatactat aagtaaatat 600
ttactagaac tgggtactta tttagatgat tcttatcgta tgatggaaca aaatacacat 660
aatatcaata agttgtctaa agaattgcaa actgggttag ccaaccaatc agcattgtct 720
atgttagtgc aaccaaattg tgtaggcaaa acgagcggtt ctgctgcggt aggagggtat 780
agagataaaa ctgcattagc cattgggtgc ggctcacgca ttactgatcg ctttaccgct 840
aaagcgggtg tagcggtcaa tacctacaat ggcggcgatg cttatgggtgc ttctgttggt 900
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<210> 18
<211> 257
<212> PRT
<213> Haemophilus ducreyi

<400> 18

Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
20 25 30

Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
210 215 220

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
225 230 235 240

Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
245 250 255

Phe